

1

Sequence listing

<110> Kaneka Corporation

5 <120> Process for producing coenzyme Q₁₀

<130> T549/QX-GT2

<150> JP P1999-237561

10 <151> 1999-08-24

<160> 2

<210> 1

15 <211> 1653

<212> DNA

<213> Saioella complicata

<400> 1

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gagattgagt tcaggacaaa gctttgatcc gtgaggtcta catcttcagc aaatcatttc 120

aaatccatat acc atg gcc tca cca gca ctg cgg ata cga agc atc agc 169

25 Met Ala Ser Pro Ala Leu Arg Ile Arg Ser Ile Ser

1

5

10

Sub B1

tct cga tca atc gcc tct ctg cga tcg gtt acc cta aga aca gcc tcg 217
 Ser Arg Ser Ile Ala Ser Leu Arg Ser Val Thr Leu Arg Thr Ala Ser
 15 20 25

5

gca cct tca tta cga cta aga tgt acc ccg acg agc cgg cca tcg agt 265
 Ala Pro Ser Leu Arg Leu Arg Cys Thr Pro Thr Ser Arg Pro Ser Ser
 30 35 40

10

tca tgg gct gct gct gtg tct tcg gcg tcg aga ctg gtt gag cct gat 313
 Ser Trp Ala Ala Ala Val Ser Ser Ala Ser Arg Leu Val Glu Pro Asp
 45 50 55 60

ccg aat caa cct ctc atc aat ccg ctc aac ttg gtc ggt ccc gag atg 361
 15 Pro Asn Gln Pro Leu Ile Asn Pro Leu Asn Leu Val Gly Pro Glu Met
 65 70 75

tca aat ctt aca tcc aac atc cga tct ctc ctc ggt tca gga cac cct 409
 Ser Asn Leu Thr Ser Asn Ile Arg Ser Leu Leu Gly Ser Gly His Pro
 20 80 85 90

tct ctc gac act gtc gct aaa tac tat gtt cag tct gag gga aag cat 457
 Ser Leu Asp Thr Val Ala Lys Tyr Tyr Val Gln Ser Glu Gly Lys His
 95 100 105

25

att cgt ccg ctc atg gta ctg ctg atg gct cag gcg acg gag gtt gcg 505

Ile Arg Pro Leu Met Val Leu Leu Met Ala Gln Ala Thr Glu Val Ala
 110 115 120

cca aaa gtt cag ggt tgg gag aag gtc gtg gag gtt ccg gtg aac gag 553
 5 Pro Lys Val Gln Gly Trp Glu Lys Val Val Glu Val Pro Val Asn Glu
 125 130 135 140

gga ctc gca cca cca gag gtg ctc aat gac aag aac cca gat atg atg 601
 Gly Leu Ala Pro Pro Glu Val Leu Asn Asp Lys Asn Pro Asp Met Met
 10 145 150 155

aac atg agg tca gga cca tta acg aag gac ggc gag atc gag gga cag 649
 Asn Met Arg Ser Gly Pro Leu Thr Lys Asp Gly Glu Ile Glu Gly Gln
 160 165 170

15 acg tcg aat atc ctc gcc tcg caa cgg cgg ttg gct gag atc acg gag 697
 Thr Ser Asn Ile Leu Ala Ser Gln Arg Arg Leu Ala Glu Ile Thr Glu
 175 180 185

20 atg atc cat gca gca tca ctc ctc cac gac gac gtt atc gac gct tcc 745
 Met Ile His Ala Ala Ser Leu Leu His Asp Asp Val Ile Asp Ala Ser
 190 195 200

gag acc aga cga aac gca cca tcc gga aac cag gca ttc gga aac aag 793
 25 Glu Thr Arg Arg Asn Ala Pro Ser Gly Asn Gln Ala Phe Gly Asn Lys
 205 210 215 220

atg gcg att ttg gct ggt gat ttc ttg ttg gga cgg gcg tct gtt gca 841
 Met Ala Ile Leu Ala Gly Asp Phe Leu Leu Gly Arg Ala Ser Val Ala
 225 230 235

5

ttg gcg agg ttg cgc aat ccg gag gtg att gag ctt ttg gct act gtt 889
 Leu Ala Arg Leu Arg Asn Pro Glu Val Ile Glu Leu Leu Ala Thr Val
 240 245 250

10

att gca aac ttg gtt gag gga gag ttc atg cag ttg aaa aat act gtt 937
 Ile Ala Asn Leu Val Glu Gly Glu Phe Met Gln Leu Lys Asn Thr Val
 255 260 265

gat gat gcg att gag gct acg gcg acg cag gaa acg ttc gat tac tat 985
 Asp Asp Ala Ile Glu Ala Thr Ala Thr Gln Glu Thr Phe Asp Tyr Tyr
 270 275 280

15

ttg cag aag act tac ttg aag act gcg tcc ttg att gcc aag tcg tgc 1033
 Leu Gln Lys Thr Tyr Leu Lys Thr Ala Ser Leu Ile Ala Lys Ser Cys
 285 290 295 300

20

aga gca agt gcg ctt ctg ggt ggt gct acg cct gag gtt gct gat gct 1081
 Arg Ala Ser Ala Leu Leu Gly Gly Ala Thr Pro Glu Val Ala Asp Ala
 305 310 315

25

gct tat gct tac gga agg aac ctt ggt ttg gca ttc cag atc gtc gac 1129

Ala Tyr Ala Tyr Gly Arg Asn Leu Gly Leu Ala Phe Gln Ile Val Asp
320 325 330

gac atg ctc gac tac acc gtc tcc gct acc gac ctc ggt aag ccc gcc 1177
5 Asp Met Leu Asp Tyr Thr Val Ser Ala Thr Asp Leu Gly Lys Pro Ala
335 340 345

ggt gca gac ctc cag ctc ggt ctc gcc acc gcg ccg gcc ctc ttc gca 1225
Gly Ala Asp Leu Gln Leu Gly Leu Ala Thr Ala Pro Ala Leu Phe Ala
10 350 355 360

tgg aag cac cac gcc gag ctc ggt ccc atg atc aag cgc aag ttc tct 1273
Trp Lys His His Ala Glu Leu Gly Pro Met Ile Lys Arg Lys Phe Ser
365 370 375 380

15 gac cca gga gac gtc gag cgt gca cgc gag ttg gtc gag aaa agt gat 1321
Asp Pro Gly Asp Val Glu Arg Ala Arg Glu Leu Val Glu Lys Ser Asp
385 390 395

20 gga ttg gag aag acg aga gcc ttg gcg gag gag tat gcc cag aag gcg 1369
Gly Leu Glu Lys Thr Arg Ala Leu Ala Glu Glu Tyr Ala Gln Lys Ala
400 405 410

ttg gat gca att cgg acg ttc ccg gag agt ccg gca cgg aag gct ttg 1417
25 Leu Asp Ala Ile Arg Thr Phe Pro Glu Ser Pro Ala Arg Lys Ala Leu
415 420 425

gag cag ttg acg gac aag gtg ttg act agg tca aga taggaattcgagct 1467

Glu Gln Leu Thr Asp Lys Val Leu Thr Arg Ser Arg

430

435

440

5

cgtacccgg ggatcctcta gagtcgacct gcaggcatgc aagcttggt gttttggcgg 1527

atgagagaag attttcagcc tgatacagat taaatcagaa cgcagaagcg gtctgataaa 1587

10 acagaatttg cctggcggca gtagecgggt ggtcccacct gaccccatgc cgaactcaga 1647

agtga

1653

15 <210> 2

<211> 440

<212> PRT

<213> Saioella complicata

20 <400> 2

Met Ala Ser Pro Ala Leu Arg Ile Arg Ser Ile Ser Ser Arg Ser

1

5

10

15

Ile Ala Ser Leu Arg Ser Val Thr Leu Arg Thr Ala Ser Ala Pro

20

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30

25 Ser Leu Arg Leu Arg Cys Thr Pro Thr Ser Arg Pro Ser Ser Ser

35

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45

	Arg Asn Pro Glu Val Ile Glu Leu Leu Ala Thr Val Ile Ala Asn		
	245	250	255
	Leu Val Glu Gly Glu Phe Met Gln Leu Lys Asn Thr Val Asp Asp		
	260	265	270
5	Ala Ile Glu Ala Thr Ala Thr Gln Glu Thr Phe Asp Tyr Tyr Leu		
	275	280	285
	Gln Lys Thr Tyr Leu Lys Thr Ala Ser Leu Ile Ala Lys Ser Cys		
	290	295	300
	Arg Ala Ser Ala Leu Leu Gly Gly Ala Thr Pro Glu Val Ala Asp		
10	305	310	315
	Ala Ala Tyr Ala Tyr Gly Arg Asn Leu Gly Leu Ala Phe Gln Ile		
	320	325	330
	Val Asp Asp Met Leu Asp Tyr Thr Val Ser Ala Thr Asp Leu Gly		
	335	340	345
15	Lys Pro Ala Gly Ala Asp Leu Gln Leu Gly Leu Ala Thr Ala Pro		
	350	355	360
	Ala Leu Phe Ala Trp Lys His His Ala Glu Leu Gly Pro Met Ile		
	365	370	375
	Lys Arg Lys Phe Ser Asp Pro Gly Asp Val Glu Arg Ala Arg Glu		
20	380	385	390
	Leu Val Glu Lys Ser Asp Gly Leu Glu Lys Thr Arg Ala Leu Ala		
	395	400	405
	Glu Glu Tyr Ala Gln Lys Ala Leu Asp Ala Ile Arg Thr Phe Pro		
	410	415	420
25	Glu Ser Pro Ala Arg Lys Ala Leu Glu Gln Leu Thr Asp Lys Val		
	425	430	435

Leu Thr Arg Ser Arg

440